

SEQUENCE LISTING

<110> Reed, John C.
 Godzik, Adam
 Pawlowski, Krzysztof
 Fiorentino, Loredana
 Lee, Sug Hyung
 Roth, Wilfred
 Stenner-Liewen, Frank

<120> Novel Death Domain Proteins

<130> P-LJ 5037

<150> 60/301,889

<151> 2001-06-29

<150> 09/715,893

<151> 2000-11-17

<160> 62

<170> FastSEQ for Windows Version 4.0

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<213> Homo sapien

<220>

<221> CDS

<222> (1)...(210)

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1				5				10						15		

ccc	gag	gaa	tta	gca	ctt	gtt	cac	aac	ttg	agg	aaa	atg	atg	aaa	aat	96
Pro	Glu	Glu	Leu	Ala	Leu	Val	His	Asn	Leu	Arg	Lys	Met	Met	Lys	Asn	
			20				25						30			

gat	tgg	cat	gga	ggc	gcc	att	gtg	tcg	gct	ttg	agc	cag	act	ggg	tct	144
Asp	Trp	His	Gly	Gly	Ala	Ile	Val	Ser	Ala	Leu	Ser	Gln	Thr	Gly	Ser	
		35				40						45				

ctc	ttt	aag	ccc	cgg	aaa	gcc	tat	ctg	ccc	cag	gag	ttg	ctg	gga	aag	192
Leu	Phe	Lys	Pro	Arg	Lys	Ala	Tyr	Leu	Pro	Gln	Glu	Leu	Leu	Gly	Lys	
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gaa	gga	ttt	gat	gcc	ctg											210
Glu	Gly	Phe	Asp	Ala	Leu											
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<210> 2
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 <212> PRT
 <213> Homo sapien

<400> 2
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 1 5 10 15
 Pro Glu Glu Leu Ala Leu Val His Asn Leu Arg Lys Met Met Lys Asn
 20 25 30
 Asp Trp His Gly Gly Ala Ile Val Ser Ala Leu Ser Gln Thr Gly Ser
 35 40 45
 Leu Phe Lys Pro Arg Lys Ala Tyr Leu Pro Gln Glu Leu Leu Gly Lys
 50 55 60
 Glu Gly Phe Asp Ala Leu
 65 70

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 <211> 297
 <212> DNA
 <213> Homo sapien

<220>
 <221> CDS
 <222> (1)...(297)

<400> 3
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 Thr Ser Phe Ala Tyr Pro Ala Ile Arg Tyr Leu Leu Tyr Gly Glu Lys
 1 5 10 15
 gga aca gga aaa acc cta agt ctt tgc cat gtt att cat ttc tgt gca 96
 Gly Thr Gly Lys Thr Leu Ser Leu Cys His Val Ile His Phe Cys Ala
 20 25 30
 aaa cag gac tgg ctg ata cta cat att cca gat gct cat ctt tgg gtg 144
 Lys Gln Asp Trp Leu Ile Leu His Ile Pro Asp Ala His Leu Trp Val
 35 40 45
 aaa aat tgt cgg gat ctt ctg cag tcc agc tac aac aaa cag cgc ttt 192
 Lys Asn Cys Arg Asp Leu Leu Gln Ser Ser Tyr Asn Lys Gln Arg Phe
 50 55 60
 gat caa cct tta gag gct tca acc tgg ctg aag aat ttc aaa act aca 240
 Asp Gln Pro Leu Glu Ala Ser Thr Trp Leu Lys Asn Phe Lys Thr Thr
 65 70 75 80
 aat gag cgc ttc ctg aac cag ata aaa gtt caa gag aag tat gtc tgg 288
 Asn Glu Arg Phe Leu Asn Gln Ile Lys Val Gln Glu Lys Tyr Val Trp
 85 90 95
 aat aag aga 297

Asn Lys Arg

<210> 4
<211> 99
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<213> Homo sapien

<400> 4
Thr Ser Phe Ala Tyr Pro Ala Ile Arg Tyr Leu Leu Tyr Gly Glu Lys
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Gly Thr Gly Lys Thr Leu Ser Leu Cys His Val Ile His Phe Cys Ala
20 25 30
Lys Gln Asp Trp Leu Ile Leu His Ile Pro Asp Ala His Leu Trp Val
35 40 45
Lys Asn Cys Arg Asp Leu Leu Gln Ser Ser Tyr Asn Lys Gln Arg Phe
50 55 60
Asp Gln Pro Leu Glu Ala Ser Thr Trp Leu Lys Asn Phe Lys Thr Thr
65 70 75 80
Asn Glu Arg Phe Leu Asn Gln Ile Lys Val Gln Glu Lys Tyr Val Trp
85 90 95
Asn Lys Arg

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<212> DNA
<213> Homo sapien

<220>
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<222> (1)...(294)

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Thr Tyr Val Arg Cys Leu Asn Val Gly Leu Ile Arg Lys Leu Ser Asp
1 5 10 15
ttt att gat cct caa gaa gga tgg aag aag tta gct gta gct att aaa 96
Phe Ile Asp Pro Gln Glu Gly Trp Lys Lys Leu Ala Val Ala Ile Lys
20 25 30
aaa cca tct ggt gat gat aga tac aat cag ttt cac ata agg aga ttt 144
Lys Pro Ser Gly Asp Asp Arg Tyr Asn Gln Phe His Ile Arg Arg Phe
35 40 45
gaa gca tta ctt caa act gga aaa agt ccc act tct gaa tta ctg ttt 192
Glu Ala Leu Leu Gln Thr Gly Lys Ser Pro Thr Ser Glu Leu Leu Phe
50 55 60
gac tgg ggc acc aca aat tgc aca gtt ggt gat ctt gtg gat ctt ttg 240
Asp Trp Gly Thr Thr Asn Cys Thr Val Gly Asp Leu Val Asp Leu Leu
65 70 75 80

atc caa aat gaa ttt ttt gct cct gcg agt ctt ttg ctc cca gat gct 288
 ile gln asn glu phe phe ala pro ala ser leu leu leu pro asp ala
 85 90 95

gtt ccc 294
 val pro

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 <212> PRT
 <213> Homo sapien

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 thr tyr val arg cys leu asn val gly leu ile arg lys leu ser asp
 1 5 10 15
 phe ile asp pro gln glu gly trp lys lys leu ala val ala ile lys
 20 25 30
 lys pro ser gly asp asp arg tyr asn gln phe his ile arg arg phe
 35 40 45
 glu ala leu leu gln thr gly lys ser pro thr ser glu leu leu phe
 50 55 60
 asp trp gly thr thr asn cys thr val gly asp leu val asp leu leu
 65 70 75 80
 ile gln asn glu phe phe ala pro ala ser leu leu leu pro asp ala
 85 90 95
 val pro

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 <212> DNA
 <213> Homo sapien

<220>
 <221> CDS
 <222> (1)...(303)

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 cgt atg ttc gag gtg gtg ggc ggg caa ctg acc gag tgc gag ctg gag 96
 arg met phe glu val val gly gly gln leu thr glu cys glu leu glu
 20 25 30
 ctc ctg gcc ttt ctg ctg gat gag gct cct ggc gcc gcc gga ggc tta 144
 leu leu ala phe leu leu asp glu ala pro gly ala ala gly gly leu
 35 40 45
 gcc cgg gcc cgc agc ggc cta gag ctc ctg ctg gag ctg gag cgc cgc 192

Ala Arg Ala Arg Ser Gly Leu Glu Leu Leu Leu Glu Leu Glu Arg Arg
50 55 60

ggg cag tgc gac gag agc aac ctg cgg ctg ctg ggg caa ctc ctg cgc 240
Gly Gln Cys Asp Glu Ser Asn Leu Arg Leu Leu Gly Gln Leu Leu Arg
65 70 75 80

gtg ctg gcc cgc cac gac ctg ctg ccg cac ctg gcg cgc aag cgg cgc 288
Val Leu Ala Arg His Asp Leu Leu Pro His Leu Ala Arg Lys Arg Arg
85 90 95

cgg cca gtg tct cca 303
Arg Pro Val Ser Pro
100

<210> 8
<211> 101
<212> PRT
<213> Homo sapien

<400> 8
Trp Glu Glu Asp Glu Cys Leu Asp Tyr Tyr Gly Met Leu Ser Leu His
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20 25 30
Leu Leu Ala Phe Leu Leu Asp Glu Ala Pro Gly Ala Ala Gly Gly Leu
35 40 45
Ala Arg Ala Arg Ser Gly Leu Glu Leu Leu Leu Glu Leu Glu Arg Arg
50 55 60
Gly Gln Cys Asp Glu Ser Asn Leu Arg Leu Leu Gly Gln Leu Leu Arg
65 70 75 80
Val Leu Ala Arg His Asp Leu Leu Pro His Leu Ala Arg Lys Arg Arg
85 90 95
Arg Pro Val Ser Pro
100

<210> 9
<211> 195
<212> DNA
<213> Chlamydia trachomatis

<220>
<221> CDS
<222> (1)...(195)

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1 5 10 15
tta gag gct cat gag cct agt gaa gca gca aaa gcg aaa gta gct act 96
Leu Glu Ala His Glu Pro Ser Glu Ala Ala Lys Ala Lys Val Ala Thr
20 25 30

ttc atg cgg tgg tgt aca gga gat tct tta gct gca gga gtg gct gct 144
Phe Met Arg Trp Cys Thr Gly Asp Ser Leu Ala Ala Gly Val Ala Ala
35 40 45

ttg tat tct tat gag agt caa att cca cgt atc gct aga gag aaa att 192
Leu Tyr Ser Tyr Glu Ser Gln Ile Pro Arg Ile Ala Arg Glu Lys Ile
50 55 60

cgt 195
Arg
65

<210> 10
<211> 65
<212> PRT
<213> Chlamydia trachomatis

<400> 10
Asp Leu Trp Lys Gln Phe Val Phe Ala Leu Gly Val Thr Pro Glu Glu
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Leu Glu Ala His Glu Pro Ser Glu Ala Ala Lys Ala Lys Val Ala Thr
20 25 30
Phe Met Arg Trp Cys Thr Gly Asp Ser Leu Ala Ala Gly Val Ala Ala
35 40 45
Leu Tyr Ser Tyr Glu Ser Gln Ile Pro Arg Ile Ala Arg Glu Lys Ile
50 55 60
Arg
65

<210> 11
<211> 213
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (1)...(213)

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Gln Gln Gln Glu Glu Val Gln Arg Leu Leu Met Met Gly Glu Pro Ala
1 5 10 15

aag ggc tgg cag gag ctg gca ggc cac ctc ggc tac caa gct gag gct 96
Lys Gly Trp Gln Glu Leu Ala Gly His Leu Gly Tyr Gln Ala Glu Ala
20 25 30

gtg gaa acc atg gcc tgt gac caa atg cca gcc tat acc ctg cta agg 144
Val Glu Thr Met Ala Cys Asp Gln Met Pro Ala Tyr Thr Leu Leu Arg
35 40 45

aac tgg gct gcc caa gaa ggc aat aga gct acc ctc aga gtg ctg gag 192

Asn Trp Ala Ala Gln Glu Gly Asn Arg Ala Thr Leu Arg Val Leu Glu
 50 55 60

gat gct ctg gct gcc ata ggc
 Asp Ala Leu Ala Ala Ile Gly
 65 70

213

<210> 12
 <211> 71
 <212> PRT
 <213> Mus musculus

<400> 12
 Gln Gln Gln Glu Glu Val Gln Arg Leu Leu Met Met Gly Glu Pro Ala
 1 5 10 15
 Lys Gly Trp Gln Glu Leu Ala Gly His Leu Gly Tyr Gln Ala Glu Ala
 20 25 30
 Val Glu Thr Met Ala Cys Asp Gln Met Pro Ala Tyr Thr Leu Leu Arg
 35 40 45
 Asn Trp Ala Ala Gln Glu Gly Asn Arg Ala Thr Leu Arg Val Leu Glu
 50 55 60
 Asp Ala Leu Ala Ala Ile Gly
 65 70

<210> 13
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 <212> DNA
 <213> Homo sapien

<220>
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 <222> (74) ... (1267)

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 Met Met Leu Lys Gly Ile Thr Arg Leu Ile Ser Arg
 1 5 10

atc cat aag ttg gac cct ggg cgt ttt tta cac atg ggg acc cag gct 157
 Ile His Lys Leu Asp Pro Gly Arg Phe Leu His Met Gly Thr Gln Ala
 15 20 25

cgc caa agc att gct gct cac cta gat aac cag gtt cca gtt gag agt 205
 Arg Gln Ser Ile Ala Ala His Leu Asp Asn Gln Val Pro Val Glu Ser
 30 35 40

ccg aga gct att tcc cgc acc aat gag aat gac ccg gcc aag cat ggg 253
 Pro Arg Ala Ile Ser Arg Thr Asn Glu Asn Asp Pro Ala Lys His Gly
 45 50 55 60

gat cag cac gag ggt cag cac tac aac atc tcc ccc cag gat ttg gag 301
 Asp Gln His Glu Gly Gln His Tyr Asn Ile Ser Pro Gln Asp Leu Glu

65										70					75					
act	gta	ttt	ccc	cat	ggc	ctt	cct	cct	cgc	ttt	gtg	atg	cag	gtg	aag	349				
Thr	Val	Phe	Pro	His	Gly	Leu	Pro	Pro	Arg	Phe	Val	Met	Gln	Val	Lys					
			80						85				90							
aca	ttc	agt	gaa	gct	tgc	ctg	atg	gta	agg	aaa	cca	gcc	cta	gaa	ctt	397				
Thr	Phe	Ser	Glu	Ala	Cys	Leu	Met	Val	Arg	Lys	Pro	Ala	Leu	Glu	Leu					
		95					100					105								
ctg	cat	tac	ctg	aaa	aac	acc	agt	ttt	gct	tat	cca	gct	ata	cga	tat	445				
Leu	His	Tyr	Leu	Lys	Asn	Thr	Ser	Phe	Ala	Tyr	Pro	Ala	Ile	Arg	Tyr					
	110					115					120									
ctt	ctg	tat	gga	gag	aag	gga	aca	gga	aaa	acc	cta	agt	ctt	tgc	cat	493				
Leu	Leu	Tyr	Gly	Glu	Lys	Gly	Thr	Gly	Lys	Thr	Leu	Ser	Leu	Cys	His					
125					130					135					140					
gtt	att	cat	ttc	tgt	gca	aaa	cag	gac	tgg	ctg	ata	cta	cat	att	cca	541				
Val	Ile	His	Phe	Cys	Ala	Lys	Gln	Asp	Trp	Leu	Ile	Leu	His	Ile	Pro					
				145				150						155						
gat	gct	cat	ctt	tgg	gtg	aaa	aat	tgt	cgg	gat	ctt	ctg	cag	tcc	agc	589				
Asp	Ala	His	Leu	Trp	Val	Lys	Asn	Cys	Arg	Asp	Leu	Leu	Gln	Ser	Ser					
			160					165					170							
tac	aac	aaa	cag	cgc	ttt	gat	caa	cct	tta	gag	gct	tca	acc	tgg	ctg	637				
Tyr	Asn	Lys	Gln	Arg	Phe	Asp	Gln	Pro	Leu	Glu	Ala	Ser	Thr	Trp	Leu					
		175					180					185								
aag	aat	ttc	aaa	act	aca	aat	gag	cgc	ttc	ctg	aac	cag	ata	aaa	gtt	685				
Lys	Asn	Phe	Lys	Thr	Thr	Asn	Glu	Arg	Phe	Leu	Asn	Gln	Ile	Lys	Val					
	190					195					200									
caa	gag	aag	tat	gtc	tgg	aat	aag	aga	gaa	agc	act	gag	aaa	ggg	agt	733				
Gln	Glu	Lys	Tyr	Val	Trp	Asn	Lys	Arg	Glu	Ser	Thr	Glu	Lys	Gly	Ser					
205					210					215					220					
cct	ctg	gga	gaa	gtg	gtt	gaa	cag	ggc	ata	aca	cgg	gtg	agg	aac	gcc	781				
Pro	Leu	Gly	Glu	Val	Val	Glu	Gln	Gly	Ile	Thr	Arg	Val	Arg	Asn	Ala					
				225				230						235						
aca	gat	gca	gtt	gga	att	gtg	ctg	aaa	gag	cta	aag	agg	caa	agt	tct	829				
Thr	Asp	Ala	Val	Gly	Ile	Val	Leu	Lys	Glu	Leu	Lys	Arg	Gln	Ser	Ser					
			240					245					250							
ttg	ggt	atg	ttt	cac	ctc	cta	gtg	gcc	gtg	gat	gga	atc	aat	gct	ctt	877				
Leu	Gly	Met	Phe	His	Leu	Leu	Val	Ala	Val	Asp	Gly	Ile	Asn	Ala	Leu					
		255					260					265								
tgg	gga	aga	acc	act	ctg	aaa	aga	gaa	gat	aaa	agc	ccg	att	gcc	ccc	925				
Trp	Gly	Arg	Thr	Thr	Leu	Lys	Arg	Glu	Asp	Lys	Ser	Pro	Ile	Ala	Pro					
		270				275					280									
gag	gaa	tta	gca	ctt	gtt	cac	aac	ttg	agg	aaa	atg	atg	aaa	aat	gat	973				

Glu Glu Leu Ala Leu Val His Asn Leu Arg Lys Met Met Lys Asn Asp
285 290 295 300

tgg cat gga ggc gcc att gtg tgc gct ttg agc cag act ggg tct ctc 1021
Trp His Gly Gly Ala Ile Val Ser Ala Leu Ser Gln Thr Gly Ser Leu
305 310 315

ttt aag ccc cgg aaa gcc tat ctg ccc cag gag ttg ctg gga aag gaa 1069
Phe Lys Pro Arg Lys Ala Tyr Leu Pro Gln Glu Leu Leu Gly Lys Glu
320 325 330

gga ttt gat gcc ctg gat ccc ttt att ccc atc ctg gtt tcc aac tat 1117
Gly Phe Asp Ala Leu Asp Pro Phe Ile Pro Ile Leu Val Ser Asn Tyr
335 340 345

aac cca aag gaa ttt gaa agt tgt att cag tat tat ttg gaa aac aat 1165
Asn Pro Lys Glu Phe Glu Ser Cys Ile Gln Tyr Tyr Leu Glu Asn Asn
350 355 360

tgg ctt caa cat gag aaa gct cct aca gaa gaa ggg aaa aaa gag ctg 1213
Trp Leu Gln His Glu Lys Ala Pro Thr Glu Glu Gly Lys Lys Glu Leu
365 370 375 380

ctg ttc cta agt aac gcg aac ccc tgc ctg ctg gag cgg cac tgt gcc 1261
Leu Phe Leu Ser Asn Ala Asn Pro Ser Leu Leu Glu Arg His Cys Ala
385 390 395

tac ctc taagccaaga tcacagcatg tgaggaagac agtggacatc tgctttatgc 1317
Tyr Leu

tggacccagt aagatgagga agtcgggcag tacacaggaa gaggagccag gcccttgtac 1377
ctatgggatt ggacaggact gcagttggct ctggacctgc attaaaatgg gtttcactgt 1437
gaatgctga caataagata ttcccttggt cctaaaactt tatatcagtt tattggatgt 1497
gggtttttcac atttaagata attatggctc ttttcctaaa aaataaaaata tcttttctaaa 1557
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1605

<210> 14
<211> 398
<212> PRT
<213> Homo sapien

<400> 14
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Asp Pro Gly Arg Phe Leu His Met Gly Thr Gln Ala Arg Gln Ser Ile
20 25 30
Ala Ala His Leu Asp Asn Gln Val Pro Val Glu Ser Pro Arg Ala Ile
35 40 45
Ser Arg Thr Asn Glu Asn Asp Pro Ala Lys His Gly Asp Gln His Glu
50 55 60
Gly Gln His Tyr Asn Ile Ser Pro Gln Asp Leu Glu Thr Val Phe Pro
65 70 75 80
His Gly Leu Pro Pro Arg Phe Val Met Gln Val Lys Thr Phe Ser Glu
85 90 95

Gly	Leu	Ile	Arg	Lys	Leu	Ser	Asp	Phe	Ile	Asp	Pro	Gln	Glu	Gly	Trp	
			20					25					30			
aag	aag	tta	gct	gta	gct	att	aaa	aaa	cca	tct	ggt	gat	gat	aga	tac	144
Lys	Lys	Leu	Ala	Val	Ala	Ile	Lys	Lys	Pro	Ser	Gly	Asp	Asp	Arg	Tyr	
		35					40					45				
aat	cag	ttt	cac	ata	agg	aga	ttt	gaa	gca	tta	ctt	caa	act	gga	aaa	192
Asn	Gln	Phe	His	Ile	Arg	Arg	Phe	Glu	Ala	Leu	Leu	Gln	Thr	Gly	Lys	
	50					55					60					
agt	ccc	act	tct	gaa	tta	ctg	ttt	gac	tgg	ggc	acc	aca	aat	tgc	aca	240
Ser	Pro	Thr	Ser	Glu	Leu	Leu	Phe	Asp	Trp	Gly	Thr	Thr	Asn	Cys	Thr	
	65				70					75					80	
gtt	ggt	gat	ctt	gtg	gat	ctt	ttg	atc	caa	aat	gaa	ttt	ttt	gct	cct	288
Val	Gly	Asp	Leu	Val	Asp	Leu	Leu	Ile	Gln	Asn	Glu	Phe	Phe	Ala	Pro	
				85				90						95		
gcg	agt	ctt	ttg	ctc	cca	gat	gct	gtt	ccc	aaa	act	gct	aat	aca	cta	336
Ala	Ser	Leu	Leu	Leu	Pro	Asp	Ala	Val	Pro	Lys	Thr	Ala	Asn	Thr	Leu	
			100					105					110			
cct	tct	aaa	gaa	gct	ata	aca	gtt	cag	caa	aaa	cag	atg	cct	ttc	tgt	384
Pro	Ser	Lys	Glu	Ala	Ile	Thr	Val	Gln	Gln	Lys	Gln	Met	Pro	Phe	Cys	
		115					120					125				
gac	aaa	gac	agg	aca	ttg	atg	aca	cct	gtg	cag	aat	ctt	gaa	caa	agc	432
Asp	Lys	Asp	Arg	Thr	Leu	Met	Thr	Pro	Val	Gln	Asn	Leu	Glu	Gln	Ser	
	130					135					140					
tat	atg	cca	cct	gac	tcc	tca	agt	cca	gaa	aat	aaa	agt	tta	gaa	gtt	480
Tyr	Met	Pro	Pro	Asp	Ser	Ser	Ser	Pro	Glu	Asn	Lys	Ser	Leu	Glu	Val	
	145				150					155					160	
agt	gat	aca	cgt	ttt	cac	agt	ttt	tca	ttt	tat	gaa	ttg	aag	aat	gtc	528
Ser	Asp	Thr	Arg	Phe	His	Ser	Phe	Ser	Phe	Tyr	Glu	Leu	Lys	Asn	Val	
				165				170						175		
aca	aat	aac	ttt	gat	gaa	cga	ccc	att	tct	gtt	ggt	ggt	aat	aaa	atg	576
Thr	Asn	Asn	Phe	Asp	Glu	Arg	Pro	Ile	Ser	Val	Gly	Gly	Asn	Lys	Met	
			180					185					190			
gga	gag	gga	gga	ttt	gga	gtt	gta	tat	aaa	ggc	tac	gta	aat	aac	aca	624
Gly	Glu	Gly	Gly	Phe	Gly	Val	Val	Tyr	Lys	Gly	Tyr	Val	Asn	Asn	Thr	
		195					200					205				
act	gtg	gca	gtg	aag	aag	ctt	gca	gca	atg	gtt	gac	att	act	act	gaa	672
Thr	Val	Ala	Val	Lys	Lys	Leu	Ala	Ala	Met	Val	Asp	Ile	Thr	Thr	Glu	
	210					215					220					
gaa	ctg	aaa	cag	cag	ttt	gat	caa	gaa	ata	aaa	gta	atg	gca	aag	tgt	720
Glu	Leu	Lys	Gln	Gln	Phe	Asp	Gln	Glu	Ile	Lys	Val	Met	Ala	Lys	Cys	
	225				230					235					240	

caa cat gaa aac tta gta gaa cta ctt ggt ttc tca agt gat gga gat	768
Gln His Glu Asn Leu Val Glu Leu Leu Gly Phe Ser Ser Asp Gly Asp	
245 250 255	
gac ctc tgc tta gta tat gtt tac atg cct aat ggt tca ttg cta gac	816
Asp Leu Cys Leu Val Tyr Val Tyr Met Pro Asn Gly Ser Leu Leu Asp	
260 265 270	
aga ctc tct tgc ttg gat ggt act cca cca ctt tct tgg cac atg aga	864
Arg Leu Ser Cys Leu Asp Gly Thr Pro Pro Leu Ser Trp His Met Arg	
275 280 285	
tgc aag att gct cag ggt gca gct aat ggc atc aat ttt cta cat gaa	912
Cys Lys Ile Ala Gln Gly Ala Ala Asn Gly Ile Asn Phe Leu His Glu	
290 295 300	
aat cat cat att cat aga gat att aaa agt gca aat atc tta ctg gat	960
Asn His His Ile His Arg Asp Ile Lys Ser Ala Asn Ile Leu Leu Asp	
305 310 315 320	
gaa gct ttt act gct aaa ata tct gac ttt ggc ctt gca cgg gct tct	1008
Glu Ala Phe Thr Ala Lys Ile Ser Asp Phe Gly Leu Ala Arg Ala Ser	
325 330 335	
gag aag ttt gcc cag aca gtc atg act agc aga att gtg gga aca aca	1056
Glu Lys Phe Ala Gln Thr Val Met Thr Ser Arg Ile Val Gly Thr Thr	
340 345 350	
gct tat atg gca cca gaa gct ttg cgt gga gaa ata aca ccc aaa tct	1104
Ala Tyr Met Ala Pro Glu Ala Leu Arg Gly Glu Ile Thr Pro Lys Ser	
355 360 365	
gat att tac agc ttt ggt gtg gtt tta cta gaa ata ata act gga ctt	1152
Asp Ile Tyr Ser Phe Gly Val Val Leu Leu Glu Ile Ile Thr Gly Leu	
370 375 380	
cca gct gtg gat gaa cac cgt gaa cct cag tta ttg cta gat att aaa	1200
Pro Ala Val Asp Glu His Arg Glu Pro Gln Leu Leu Leu Asp Ile Lys	
385 390 395 400	
gaa gaa att gaa gat gaa gaa aag aca att gaa gat tat att gat aaa	1248
Glu Glu Ile Glu Asp Glu Glu Lys Thr Ile Glu Asp Tyr Ile Asp Lys	
405 410 415	
aag atg aat gat gct gat tcc act tca gtt gaa gct atg tac tct gtt	1296
Lys Met Asn Asp Ala Asp Ser Thr Ser Val Glu Ala Met Tyr Ser Val	
420 425 430	
gct agt caa tgt ctg cat gaa aag aaa aat aag aga cca gac att aag	1344
Ala Ser Gln Cys Leu His Glu Lys Lys Asn Lys Arg Pro Asp Ile Lys	
435 440 445	
aag gtt caa cag ctg ctg caa gag atg aca gct tct taa	1383
Lys Val Gln Gln Leu Leu Glu Met Thr Ala Ser	
450 455 460	

<210> 16
 <211> 460
 <212> PRT
 <213> Homo sapien

<400> 16

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			20					25					30		
Lys	Lys	Leu	Ala	Val	Ala	Ile	Lys	Lys	Pro	Ser	Gly	Asp	Asp	Arg	Tyr
		35					40					45			
Asn	Gln	Phe	His	Ile	Arg	Arg	Phe	Glu	Ala	Leu	Leu	Gln	Thr	Gly	Lys
	50					55					60				
Ser	Pro	Thr	Ser	Glu	Leu	Leu	Phe	Asp	Trp	Gly	Thr	Thr	Asn	Cys	Thr
65					70					75					80
Val	Gly	Asp	Leu	Val	Asp	Leu	Leu	Ile	Gln	Asn	Glu	Phe	Phe	Ala	Pro
				85					90					95	
Ala	Ser	Leu	Leu	Leu	Pro	Asp	Ala	Val	Pro	Lys	Thr	Ala	Asn	Thr	Leu
			100					105						110	
Pro	Ser	Lys	Glu	Ala	Ile	Thr	Val	Gln	Gln	Lys	Gln	Met	Pro	Phe	Cys
		115					120					125			
Asp	Lys	Asp	Arg	Thr	Leu	Met	Thr	Pro	Val	Gln	Asn	Leu	Glu	Gln	Ser
	130					135					140				
Tyr	Met	Pro	Pro	Asp	Ser	Ser	Ser	Pro	Glu	Asn	Lys	Ser	Leu	Glu	Val
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Ser	Asp	Thr	Arg	Phe	His	Ser	Phe	Ser	Phe	Tyr	Glu	Leu	Lys	Asn	Val
				165					170					175	
Thr	Asn	Asn	Phe	Asp	Glu	Arg	Pro	Ile	Ser	Val	Gly	Gly	Asn	Lys	Met
			180					185					190		
Gly	Glu	Gly	Gly	Phe	Gly	Val	Val	Tyr	Lys	Gly	Tyr	Val	Asn	Asn	Thr
		195					200					205			
Thr	Val	Ala	Val	Lys	Lys	Leu	Ala	Ala	Met	Val	Asp	Ile	Thr	Thr	Glu
	210					215					220				
Glu	Leu	Lys	Gln	Gln	Phe	Asp	Gln	Glu	Ile	Lys	Val	Met	Ala	Lys	Cys
225					230					235					240
Gln	His	Glu	Asn	Leu	Val	Glu	Leu	Leu	Gly	Phe	Ser	Ser	Asp	Gly	Asp
				245					250					255	
Asp	Leu	Cys	Leu	Val	Tyr	Val	Tyr	Met	Pro	Asn	Gly	Ser	Leu	Leu	Asp
			260					265					270		
Arg	Leu	Ser	Cys	Leu	Asp	Gly	Thr	Pro	Pro	Leu	Ser	Trp	His	Met	Arg
		275					280					285			
Cys	Lys	Ile	Ala	Gln	Gly	Ala	Ala	Asn	Gly	Ile	Asn	Phe	Leu	His	Glu
	290					295					300				
Asn	His	His	Ile	His	Arg	Asp	Ile	Lys	Ser	Ala	Asn	Ile	Leu	Leu	Asp
305					310					315					320
Glu	Ala	Phe	Thr	Ala	Lys	Ile	Ser	Asp	Phe	Gly	Leu	Ala	Arg	Ala	Ser
				325					330					335	
Glu	Lys	Phe	Ala	Gln	Thr	Val	Met	Thr	Ser	Arg	Ile	Val	Gly	Thr	Thr
			340					345					350		
Ala	Tyr	Met	Ala	Pro	Glu	Ala	Leu	Arg	Gly	Glu	Ile	Thr	Pro	Lys	Ser
		355					360					365			
Asp	Ile	Tyr	Ser	Phe	Gly	Val	Val	Leu	Leu	Glu	Ile	Ile	Thr	Gly	Leu

370	375	380
Pro Ala Val Asp Glu His	Arg Glu Pro Gln Leu	Leu Leu Asp Ile Lys
385	390	395
Glu Glu Ile Glu Asp Glu	Lys Thr Ile Glu Asp	Tyr Ile Asp Lys
405	410	415
Lys Met Asn Asp Ala Asp	Ser Thr Ser Val Glu	Ala Met Tyr Ser Val
420	425	430
Ala Ser Gln Cys Leu His	Glu Lys Lys Asn Lys	Arg Pro Asp Ile Lys
435	440	445
Lys Val Gln Gln Leu Leu	Gln Glu Met Thr Ala	Ser
450	455	460

<210> 17
 <211> 1924
 <212> DNA
 <213> Homo sapien

<220>
 <221> CDS
 <222> (91)...(1044)

<221> misc_feature
 <222> (1)...(1900)
 <223> n = A,T,C or G

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 ctgagcttgt tccgctctcc tccccggga atg gcg cta tcc ggg tcg acc ccg 114
 Met Ala Leu Ser Gly Ser Thr Pro
 1 5

gcc ccg tgc tgg gag gag gat gag tgc ctg gac tac tac ggg atg ctg 162
 Ala Pro Cys Trp Glu Glu Asp Glu Cys Leu Asp Tyr Tyr Gly Met Leu
 10 15 20

tcg ctt cac cgt atg ttc gag gtg gtg ggc ggg caa ctg acc gag tgc 210
 Ser Leu His Arg Met Phe Glu Val Val Gly Gly Gln Leu Thr Glu Cys
 25 30 35 40

gag ctg gag ctc ctg gcc ttt ctg ctg gat gag gct cct ggc gcc gcc 258
 Glu Leu Glu Leu Leu Ala Phe Leu Leu Asp Glu Ala Pro Gly Ala Ala
 45 50 55

gga ggc tta gcc cgg gcc cgc agc ggc cta gag ctc ctg ctg gag ctg 306
 Gly Gly Leu Ala Arg Ala Arg Ser Gly Leu Glu Leu Leu Leu Glu Leu
 60 65 70

gag cgc cgc ggg cag tgc gac gag agc aac ctg cgg ctg ctg ggg caa 354
 Glu Arg Arg Gly Gln Cys Asp Glu Ser Asn Leu Arg Leu Leu Gly Gln
 75 80 85

ctc ctg cgc gtg ctg gcc cgc cac gac ctg ctg ccg cac ctg gcg cgc 402
 Leu Leu Arg Val Leu Ala Arg His Asp Leu Leu Pro His Leu Ala Arg
 90 95 100

aag cgg cgc cgg cca gtg tct cca gaa cgc tat agc tat ggc acc tcc	450
Lys Arg Arg Arg Pro Val Ser Pro Glu Arg Tyr Ser Tyr Gly Thr Ser	
105 110 115 120	
agc tct tca aag agg aca gag ggt agc tgc cgt cgc cgt cgg cag tca	498
Ser Ser Ser Lys Arg Thr Glu Gly Ser Cys Arg Arg Arg Arg Gln Ser	
125 130 135	
agc agt tct gca aat tct cag cag ggt cag tgg gag aca ggc tcc ccc	546
Ser Ser Ser Ala Asn Ser Gln Gln Gly Gln Trp Glu Thr Gly Ser Pro	
140 145 150	
cca acc aag cgg cag cgg cgg agt cgg ggc cgg ccc agt ggt ggt gcc	594
Pro Thr Lys Arg Gln Arg Arg Ser Arg Gly Arg Pro Ser Gly Gly Ala	
155 160 165	
aga cgg cgg cgg aga ggg gcc cca gcc gca ccc cag cag cag tca gag	642
Arg Arg Arg Arg Arg Gly Ala Pro Ala Ala Pro Gln Gln Gln Ser Glu	
170 175 180	
ccc gcc aga cct tcc tct gaa ggc aaa gtg acc tgt gac atc cgg ctc	690
Pro Ala Arg Pro Ser Ser Glu Gly Lys Val Thr Cys Asp Ile Arg Leu	
185 190 195 200	
cgg gtt cga gca gag tac tgc gag cat ggg cca gcc ttg gag cag ggc	738
Arg Val Arg Ala Glu Tyr Cys Glu His Gly Pro Ala Leu Glu Gln Gly	
205 210 215	
gtg gca tcc cgg cgg ccc cag gcg ctg gcg cgg cag ctg gac gtg ttt	786
Val Ala Ser Arg Arg Pro Gln Ala Leu Ala Arg Gln Leu Asp Val Phe	
220 225 230	
ggg cag gcc acc gca gtg ctg cgc tca agg gac ctg ggc tct gtg gtt	834
Gly Gln Ala Thr Ala Val Leu Arg Ser Arg Asp Leu Gly Ser Val Val	
235 240 245	
tgt gac atc aag ttc tca gag ctc tcc tat ctg gac gcc ttc tgg ggc	882
Cys Asp Ile Lys Phe Ser Glu Leu Ser Tyr Leu Asp Ala Phe Trp Gly	
250 255 260	
gac tac ctg agt ggc gcc ctg ctg cag gcc ctg cgg ggc gtg ttc ctg	930
Asp Tyr Leu Ser Gly Ala Leu Leu Gln Ala Leu Arg Gly Val Phe Leu	
265 270 275 280	
act gag gcc ctg cga gag gct gtg ggc cgg gag gct gtt cgc ctg ctg	978
Thr Glu Ala Leu Arg Glu Ala Val Gly Arg Glu Ala Val Arg Leu Leu	
285 290 295	
gtc agt gtg gat gag gct gac tat gag gct ggc cgg cgc cgc ctg ttg	1026
Val Ser Val Asp Glu Ala Asp Tyr Glu Ala Gly Arg Arg Arg Leu Leu	
300 305 310	
ctg atg gag gag gaa ggg gggcgggcgcc cgacagaggc ctcctgatcc	1074
Leu Met Glu Glu Glu Gly	

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aggactggca ggattgatcc cacctccaag tctccgggcc accttctcct gggaggacga 1134
ccatctctac ccctagagga ctgtcactct agcatctttg aggactgcga caggaccggg 1194
acagcaggcc ccttgacagc cctcccaca ggatgtgggc tctgaggcct aaaccatttc 1254
cagctgagtt tccttcccag actcctccta ccccagggtg gcccattcg cctccggacg 1314
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aaaaaaaaa 1924

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<210> 18
<211> 318
<212> PRT
<213> Homo sapien

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<400> 18
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Cys Leu Asp Tyr Tyr Gly Met Leu Ser Leu His Arg Met Phe Glu Val
  20      25      30
Val Gly Gly Gln Leu Thr Glu Cys Glu Leu Glu Leu Ala Phe Leu
  35      40      45
Leu Asp Glu Ala Pro Gly Ala Ala Gly Gly Leu Ala Arg Ala Arg Ser
  50      55      60
Gly Leu Glu Leu Leu Leu Glu Leu Glu Arg Arg Gly Gln Cys Asp Glu
  65      70      75      80
Ser Asn Leu Arg Leu Leu Gly Gln Leu Leu Arg Val Leu Ala Arg His
  85      90      95
Asp Leu Leu Pro His Leu Ala Arg Lys Arg Arg Arg Pro Val Ser Pro
  100     105     110
Glu Arg Tyr Ser Tyr Gly Thr Ser Ser Ser Lys Arg Thr Glu Gly
  115     120     125
Ser Cys Arg Arg Arg Arg Gln Ser Ser Ser Ser Ala Asn Ser Gln Gln
  130     135     140
Gly Gln Trp Glu Thr Gly Ser Pro Pro Thr Lys Arg Gln Arg Arg Ser
  145     150     155     160
Arg Gly Arg Pro Ser Gly Gly Ala Arg Arg Arg Arg Gly Ala Pro
  165     170     175
Ala Ala Pro Gln Gln Gln Ser Glu Pro Ala Arg Pro Ser Ser Glu Gly
  180     185     190
Lys Val Thr Cys Asp Ile Arg Leu Arg Val Arg Ala Glu Tyr Cys Glu
  195     200     205
His Gly Pro Ala Leu Glu Gln Gly Val Ala Ser Arg Arg Pro Gln Ala
  210     215     220
Leu Ala Arg Gln Leu Asp Val Phe Gly Gln Ala Thr Ala Val Leu Arg
  225     230     235     240
Ser Arg Asp Leu Gly Ser Val Val Cys Asp Ile Lys Phe Ser Glu Leu

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				245					250					255			
Ser	Tyr	Leu	Asp	Ala	Phe	Trp	Gly	Asp	Tyr	Leu	Ser	Gly	Ala	Leu	Leu		
			260					265						270			
Gln	Ala	Leu	Arg	Gly	Val	Phe	Leu	Thr	Glu	Ala	Leu	Arg	Glu	Ala	Val		
		275					280					285					
Gly	Arg	Glu	Ala	Val	Arg	Leu	Leu	Val	Ser	Val	Asp	Glu	Ala	Asp	Tyr		
	290					295					300						
Glu	Ala	Gly	Arg	Arg	Arg	Leu	Leu	Leu	Met	Glu	Glu	Glu	Gly				
305					310					315							

<210> 19
 <211> 696
 <212> DNA
 <213> Chlamydia trachomatis

<220>
 <221> CDS
 <222> (1)...(693)

<400> 19

atg	atg	gag	gtg	ttt	atg	aat	ttt	tta	gat	cag	tta	gat	tta	att	att	48
Met	Met	Glu	Val	Phe	Met	Asn	Phe	Leu	Asp	Gln	Leu	Asp	Leu	Ile	Ile	
1			5					10					15			
caa	aat	aag	cat	atg	cta	gaa	cac	acg	ttt	tat	gtg	aaa	tgg	tcg	aag	96
Gln	Asn	Lys	His	Met	Leu	Glu	His	Thr	Phe	Tyr	Val	Lys	Trp	Ser	Lys	
			20					25					30			
ggg	gag	ctt	act	aaa	gag	caa	tta	cag	gcg	tat	gcc	aaa	gac	tat	tat	144
Gly	Glu	Leu	Thr	Lys	Glu	Gln	Leu	Gln	Ala	Tyr	Ala	Lys	Asp	Tyr	Tyr	
		35				40						45				
tta	cat	atc	aaa	gcc	ttt	cct	aaa	tat	tta	tct	gcg	att	cat	agt	cgt	192
Leu	His	Ile	Lys	Ala	Phe	Pro	Lys	Tyr	Leu	Ser	Ala	Ile	His	Ser	Arg	
	50					55					60					
tgc	gat	gat	tta	gag	gcg	cgt	aag	tta	ttg	tta	gat	aac	ttg	atg	gat	240
Cys	Asp	Asp	Leu	Glu	Ala	Arg	Lys	Leu	Leu	Leu	Asp	Asn	Leu	Met	Asp	
65					70					75				80		
gaa	gag	aac	ggt	tac	cct	aat	cat	att	gat	ttg	tgg	aag	cag	ttt	gtg	288
Glu	Glu	Asn	Gly	Tyr	Pro	Asn	His	Ile	Asp	Leu	Trp	Lys	Gln	Phe	Val	
			85						90					95		
ttt	gct	cta	gga	gtt	act	cca	gaa	gag	tta	gag	gct	cat	gag	cct	agt	336
Phe	Ala	Leu	Gly	Val	Thr	Pro	Glu	Glu	Leu	Glu	Ala	His	Glu	Pro	Ser	
		100					105						110			
gaa	gca	gca	aaa	gcg	aaa	gta	gct	act	ttc	atg	cgg	tgg	tgt	aca	gga	384
Glu	Ala	Ala	Lys	Ala	Lys	Val	Ala	Thr	Phe	Met	Arg	Trp	Cys	Thr	Gly	
		115				120						125				
gat	tct	tta	gct	gca	gga	gtg	gct	gct	ttg	tat	tct	tat	gag	agt	caa	432
Asp	Ser	Leu	Ala	Ala	Gly	Val	Ala	Ala	Leu	Tyr	Ser	Tyr	Glu	Ser	Gln	

130

135

140

att cca cgt atc gct aga gag aaa att cgt gga ttg act gag tac ttt 480
 ile Pro Arg ile Ala Arg Glu Lys ile Arg Gly Leu Thr Glu Tyr Phe
 145 150 155 160

gga ttt tcc aat cct gaa gac tat gca tat ttc aca gaa cat gaa gaa 528
 Gly Phe Ser Asn Pro Glu Asp Tyr Ala Tyr Phe Thr Glu His Glu Glu
 165 170 175

gcg gat gtg cgg cat gct aga gaa gaa aaa gcg ctc att gag atg ctt 576
 Ala Asp Val Arg His Ala Arg Glu Glu Lys Ala Leu ile Glu Met Leu
 180 185 190

ctc aaa gat gac gct gat aaa gtg tta gag gca tcg cag gaa gta acg 624
 Leu Lys Asp Asp Ala Asp Lys Val Leu Glu Ala Ser Gln Glu Val Thr
 195 200 205

caa tct ttg tat ggc ttt tta gat tct ttt ttg gat cca cga act tgt 672
 Gln Ser Leu Tyr Gly Phe Leu Asp Ser Phe Leu Asp Pro Arg Thr Cys
 210 215 220

tgt agt tgt cat caa tct tat taa 696
 Cys Ser Cys His Gln Ser Tyr
 225 230

<210> 20

<211> 231

<212> PRT

<213> Chlamydia trachomatis

<400> 20

Met Met Glu Val Phe Met Asn Phe Leu Asp Gln Leu Asp Leu ile ile
 1 5 10 15
 Gln Asn Lys His Met Leu Glu His Thr Phe Tyr Val Lys Trp Ser Lys
 20 25 30
 Gly Glu Leu Thr Lys Glu Gln Leu Gln Ala Tyr Ala Lys Asp Tyr Tyr
 35 40 45
 Leu His ile Lys Ala Phe Pro Lys Tyr Leu Ser Ala ile His Ser Arg
 50 55 60
 Cys Asp Asp Leu Glu Ala Arg Lys Leu Leu Leu Asp Asn Leu Met Asp
 65 70 75 80
 Glu Glu Asn Gly Tyr Pro Asn His ile Asp Leu Trp Lys Gln Phe Val
 85 90 95
 Phe Ala Leu Gly Val Thr Pro Glu Glu Leu Glu Ala His Glu Pro Ser
 100 105 110
 Glu Ala Ala Lys Ala Lys Val Ala Thr Phe Met Arg Trp Cys Thr Gly
 115 120 125
 Asp Ser Leu Ala Ala Gly Val Ala Ala Leu Tyr Ser Tyr Glu Ser Gln
 130 135 140
 ile Pro Arg ile Ala Arg Glu Lys ile Arg Gly Leu Thr Glu Tyr Phe
 145 150 155 160
 Gly Phe Ser Asn Pro Glu Asp Tyr Ala Tyr Phe Thr Glu His Glu Glu
 165 170 175

Ala Asp Val Arg His Ala Arg Glu Glu Lys Ala Leu Ile Glu Met Leu
 180 185 190
 Leu Lys Asp Asp Ala Asp Lys Val Leu Glu Ala Ser Gln Glu Val Thr
 195 200 205
 Gln Ser Leu Tyr Gly Phe Leu Asp Ser Phe Leu Asp Pro Arg Thr Cys
 210 215 220
 Cys Ser Cys His Gln Ser Tyr
 225 230

<210> 21
 <211> 687
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (1)...(684)

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 1 5 10 15
 cag ggg cag gac ggg gac agg gaa gga atg tgg gta gga gct ggg gga 96
 Gln Gly Gln Asp Gly Asp Arg Glu Gly Met Trp Val Gly Ala Gly Gly
 20 25 30
 gcc cta gcc ccc aat acc tcc tcc cta ttt ccc cct gag cct cca ggg 144
 Ala Leu Ala Pro Asn Thr Ser Ser Leu Phe Pro Pro Glu Pro Pro Gly
 35 40 45
 gcc tcg agc aac atc att cct gtc tac tgt gct ctc cta gct aca gtg 192
 Ala Ser Ser Asn Ile Ile Pro Val Tyr Cys Ala Leu Leu Ala Thr Val
 50 55 60
 atc ctt ggt ctg ctg gcc tat gtg gcc ttc aaa tgc tgg cgc tca cat 240
 Ile Leu Gly Leu Leu Ala Tyr Val Ala Phe Lys Cys Trp Arg Ser His
 65 70 75 80
 aag caa agg caa cag ttg gct aaa gct cgg act gta gag cta ggg gac 288
 Lys Gln Arg Gln Gln Leu Ala Lys Ala Arg Thr Val Glu Leu Gly Asp
 85 90 95
 cct gac agg gac cag agg cgt ggt gac agc aac gtc ttc gtg gac tct 336
 Pro Asp Arg Asp Gln Arg Arg Gly Asp Ser Asn Val Phe Val Asp Ser
 100 105 110
 cct cct agt ctg gag ccc tgt att ccc agc cag gga cca cac ccg gac 384
 Pro Pro Ser Leu Glu Pro Cys Ile Pro Ser Gln Gly Pro His Pro Asp
 115 120 125
 ctt ggc tgc cag ctt tac ctg cat att cca cag cag cag gag gaa 432
 Leu Gly Cys Gln Leu Tyr Leu His Ile Pro Gln Gln Gln Glu Glu
 130 135 140

gtc cag cgg ctc ctg atg atg ggt gag cca gcc aag ggc tgg cag gag 480
 Val Gln Arg Leu Leu Met Met Gly Glu Pro Ala Lys Gly Trp Gln Glu
 145 150 155 160

ctg gca ggc cac ctc ggc tac caa gct gag gct gtg gaa acc atg gcc 528
 Leu Ala Gly His Leu Gly Tyr Gln Ala Glu Ala Val Glu Thr Met Ala
 165 170 175

tgt gac caa atg cca gcc tat acc ctg cta agg aac tgg gct gcc caa 576
 Cys Asp Gln Met Pro Ala Tyr Thr Leu Leu Arg Asn Trp Ala Ala Gln
 180 185 190

gaa ggc aat aga gct acc ctc aga gtg ctg gag gat gct ctg gct gcc 624
 Glu Gly Asn Arg Ala Thr Leu Arg Val Leu Glu Asp Ala Leu Ala Ala
 195 200 205

ata ggc cga gaa gat gtg gtc cag gtt ttg agc tcg cca gct gag agc 672
 Ile Gly Arg Glu Asp Val Val Gln Val Leu Ser Ser Pro Ala Glu Ser
 210 215 220

tcc tcg gtg gtg tga 687
 Ser Ser Val Val
 225

<210> 22
 <211> 228
 <212> PRT
 <213> Mus musculus

<400> 22
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 20 25 30
 Ala Leu Ala Pro Asn Thr Ser Ser Leu Phe Pro Pro Glu Pro Pro Gly
 35 40 45
 Ala Ser Ser Asn Ile Ile Pro Val Tyr Cys Ala Leu Leu Ala Thr Val
 50 55 60
 Ile Leu Gly Leu Leu Ala Tyr Val Ala Phe Lys Cys Trp Arg Ser His
 65 70 75 80
 Lys Gln Arg Gln Gln Leu Ala Lys Ala Arg Thr Val Glu Leu Gly Asp
 85 90 95
 Pro Asp Arg Asp Gln Arg Arg Gly Asp Ser Asn Val Phe Val Asp Ser
 100 105 110
 Pro Pro Ser Leu Glu Pro Cys Ile Pro Ser Gln Gly Pro His Pro Asp
 115 120 125
 Leu Gly Cys Gln Leu Tyr Leu His Ile Pro Gln Gln Gln Glu Glu
 130 135 140
 Val Gln Arg Leu Leu Met Gly Glu Pro Ala Lys Gly Trp Gln Glu
 145 150 155 160
 Leu Ala Gly His Leu Gly Tyr Gln Ala Glu Ala Val Glu Thr Met Ala
 165 170 175
 Cys Asp Gln Met Pro Ala Tyr Thr Leu Leu Arg Asn Trp Ala Ala Gln

		180					185				190			
Glu	Gly	Asn	Arg	Ala	Thr	Leu	Arg	Val	Leu	Glu	Asp	Ala	Leu	Ala
		195					200					205		
Ile	Gly	Arg	Glu	Asp	Val	Val	Gln	Val	Leu	Ser	Ser	Pro	Ala	Glu
		210				215					220			Ser
Ser	Ser	Val	Val											
225														

<210> 23
 <211> 696
 <212> DNA
 <213> Chlamydia trachomatis

<220>
 <221> CDS
 <222> (1)...(693)

<400> 23

atg	atg	gag	gtg	ttt	atg	aat	ttt	tta	gat	cag	tta	gat	tta	att	att	48
Met	Met	Glu	Val	Phe	Met	Asn	Phe	Leu	Asp	Gln	Leu	Asp	Leu	Ile	Ile	
1			5					10				15				
caa	aat	aag	cat	atg	cta	gaa	cac	aca	ttt	tat	gtg	aaa	tgg	tcg	aag	96
Gln	Asn	Lys	His	Met	Leu	Glu	His	Thr	Phe	Tyr	Val	Lys	Trp	Ser	Lys	
			20					25				30				
ggg	gag	ctt	act	aaa	gag	caa	tta	cag	gcg	tat	gcc	aaa	gac	tat	tat	144
Gly	Glu	Leu	Thr	Lys	Glu	Gln	Leu	Gln	Ala	Tyr	Ala	Lys	Asp	Tyr	Tyr	
		35				40					45					
tta	cat	atc	aaa	gcc	ttt	cct	aaa	tat	tta	tct	gcg	att	cat	agt	cgt	192
Leu	His	Ile	Lys	Ala	Phe	Pro	Lys	Tyr	Leu	Ser	Ala	Ile	His	Ser	Arg	
	50					55					60					
tgc	gat	gat	tta	gag	gcg	cgt	aag	tta	ttg	tta	gat	aac	ttg	atg	gat	240
Cys	Asp	Asp	Leu	Glu	Ala	Arg	Lys	Leu	Leu	Leu	Asp	Asn	Leu	Met	Asp	
65				70					75				80			
gaa	gag	aac	ggt	tac	cct	aat	cat	att	gat	ttg	tgg	aag	cag	ttt	gtg	288
Glu	Glu	Asn	Gly	Tyr	Pro	Asn	His	Ile	Asp	Leu	Trp	Lys	Gln	Phe	Val	
			85						90				95			
ttt	gct	cta	gga	gtt	act	cca	gaa	gag	tta	gag	gct	cat	gag	cct	agt	336
Phe	Ala	Leu	Gly	Val	Thr	Pro	Glu	Glu	Leu	Glu	Ala	His	Glu	Pro	Ser	
		100					105				110					
gaa	gca	gca	aaa	gcg	aaa	gta	gct	act	ttc	atg	cgg	tgg	tgt	aca	gga	384
Glu	Ala	Ala	Lys	Ala	Lys	Val	Ala	Thr	Phe	Met	Arg	Trp	Cys	Thr	Gly	
		115				120					125					
gat	tct	tta	gct	gca	gga	gtg	gct	gct	ttg	tat	tct	tat	gag	agt	caa	432
Asp	Ser	Leu	Ala	Ala	Gly	Val	Ala	Ala	Leu	Tyr	Ser	Tyr	Glu	Ser	Gln	
	130				135				140							

att cca cgt atc gct aga gag aaa att cgt gga ttg act gag tac ttt 480
 Ile Pro Arg Ile Ala Arg Glu Lys Ile Arg Gly Leu Thr Glu Tyr Phe
 145 150 155 160

gga ttt tcc aat cct gaa gac tat gca tat ttc aca gaa cat gaa gaa 528
 Gly Phe Ser Asn Pro Glu Asp Tyr Ala Tyr Phe Thr Glu His Glu Glu
 165 170 175

gcg gat gtg cgg cat gct aga gaa gaa aaa gcg ctc att gag atg ctt 576
 Ala Asp Val Arg His Ala Arg Glu Glu Lys Ala Leu Ile Glu Met Leu
 180 185 190

ctc aaa gat gac gct gat aaa gtg tta gag gca tcg caa gaa gta acg 624
 Leu Lys Asp Asp Ala Asp Lys Val Leu Glu Ala Ser Gln Glu Val Thr
 195 200 205

caa tct ttg tat ggc ttt tta gat tct ttt ttg gat cca gga act tgt 672
 Gln Ser Leu Tyr Gly Phe Leu Asp Ser Phe Leu Asp Pro Gly Thr Cys
 210 215 220

tgt agt tgt cat caa tct tat taa 696
 Cys Ser Cys His Gln Ser Tyr
 225 230

<210> 24
 <211> 231
 <212> PRT
 <213> Chlamydia trachomatis

<400> 24
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 Gln Asn Lys His Met Leu Glu His Thr Phe Tyr Val Lys Trp Ser Lys
 20 25 30
 Gly Glu Leu Thr Lys Glu Gln Leu Gln Ala Tyr Ala Lys Asp Tyr Tyr
 35 40 45
 Leu His Ile Lys Ala Phe Pro Lys Tyr Leu Ser Ala Ile His Ser Arg
 50 55 60
 Cys Asp Asp Leu Glu Ala Arg Lys Leu Leu Leu Asp Asn Leu Met Asp
 65 70 75 80
 Glu Glu Asn Gly Tyr Pro Asn His Ile Asp Leu Trp Lys Gln Phe Val
 85 90 95
 Phe Ala Leu Gly Val Thr Pro Glu Glu Leu Glu Ala His Glu Pro Ser
 100 105 110
 Glu Ala Ala Lys Ala Lys Val Ala Thr Phe Met Arg Trp Cys Thr Gly
 115 120 125
 Asp Ser Leu Ala Ala Gly Val Ala Ala Leu Tyr Ser Tyr Glu Ser Gln
 130 135 140
 Ile Pro Arg Ile Ala Arg Glu Lys Ile Arg Gly Leu Thr Glu Tyr Phe
 145 150 155 160
 Gly Phe Ser Asn Pro Glu Asp Tyr Ala Tyr Phe Thr Glu His Glu Glu
 165 170 175
 Ala Asp Val Arg His Ala Arg Glu Glu Lys Ala Leu Ile Glu Met Leu
 180 185 190

Leu Lys Asp Asp Ala Asp Lys Val Leu Glu Ala Ser Gln Glu Val Thr
 195 200 205
 Gln Ser Leu Tyr Gly Phe Leu Asp Ser Phe Leu Asp Pro Gly Thr Cys
 210 215 220
 Cys Ser Cys His Gln Ser Tyr
 225 230

<210> 25
 <211> 211
 <212> DNA
 <213> Homo sapien

<220>
 <221> CDS
 <222> (1)...(177)

<400> 25
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 Met Asn Lys Pro Ile Thr Pro Ser Thr Tyr Val Arg Cys Leu Asn Val
 1 5 10 15
 gga cta att agg aag ctg tca gat ttt att gat cct caa gaa gga tgg 96
 Gly Leu Ile Arg Lys Leu Ser Asp Phe Ile Asp Pro Gln Glu Gly Trp
 20 25 30
 aag aag tta gct gta gct att aaa aaa cca tct ggt gat gat aga tac 144
 Lys Lys Leu Ala Val Ala Ile Lys Lys Pro Ser Gly Asp Asp Arg Tyr
 35 40 45
 aat cag ttt cac ata aga tgc tgt tcc caa aac taatacacta ccttctaaag 197
 Asn Gln Phe His Ile Arg Cys Cys Ser Gln Asn
 50 55
 aagctataac agtt 211

<210> 26
 <211> 59
 <212> PRT
 <213> Homo sapien

<400> 26
 Met Asn Lys Pro Ile Thr Pro Ser Thr Tyr Val Arg Cys Leu Asn Val
 1 5 10 15
 Gly Leu Ile Arg Lys Leu Ser Asp Phe Ile Asp Pro Gln Glu Gly Trp
 20 25 30
 Lys Lys Leu Ala Val Ala Ile Lys Lys Pro Ser Gly Asp Asp Arg Tyr
 35 40 45
 Asn Gln Phe His Ile Arg Cys Cys Ser Gln Asn
 50 55

<210> 27
 <211> 2817
 <212> DNA

<213> Homo sapien

<220>

<221> CDS

<222> (50)...(1429)

<400> 27

gtttcttctgt cgccggcttc agcagcccgc gcccgggcag gaatagaag atg aac aaa 58

Met Asn Lys

1

ccc ata aca cca tca aca tat gtg cgc tgc ctc aat gtt gga cta att 106

Pro Ile Thr Pro Ser Thr Tyr Val Arg Cys Leu Asn Val Gly Leu Ile

5

10

15

agg aag ctg tca gat ttt att gat cct caa gaa gga tgg aag aag tta 154

Arg Lys Leu Ser Asp Phe Ile Asp Pro Gln Glu Gly Trp Lys Lys Leu

20

25

30

35

gct gta gct att aaa aaa cca tct ggt gat gat aga tac aat cag ttt 202

Ala Val Ala Ile Lys Lys Pro Ser Gly Asp Asp Arg Tyr Asn Gln Phe

40

45

50

cac ata agg aga ttt gaa gca tta ctt caa act gga aaa agt ccc act 250

His Ile Arg Arg Phe Glu Ala Leu Leu Gln Thr Gly Lys Ser Pro Thr

55

60

65

tct gaa tta ctg ttt gac tgg ggc acc aca aat tgc aca gtt ggt gat 298

Ser Glu Leu Leu Phe Asp Trp Gly Thr Thr Asn Cys Thr Val Gly Asp

70

75

80

ctt gtg gat ctt ttg atc caa aat gaa ttt ttt gct cct gcg agt ctt 346

Leu Val Asp Leu Leu Ile Gln Asn Glu Phe Phe Ala Pro Ala Ser Leu

85

90

95

ttg ctc cca gat gct gtt ccc aaa act gct aat aca cta cct tct aaa 394

Leu Leu Pro Asp Ala Val Pro Lys Thr Ala Asn Thr Leu Pro Ser Lys

100

105

110

115

gaa gct ata aca gtt cag caa aaa cag atg cct ttc tgt gac aaa gac 442

Glu Ala Ile Thr Val Gln Gln Lys Gln Met Pro Phe Cys Asp Lys Asp

120

125

130

agg aca ttg atg aca cct gtg cag aat ctt gaa caa agc tat atg cca 490

Arg Thr Leu Met Thr Pro Val Gln Asn Leu Glu Gln Ser Tyr Met Pro

135

140

145

cct gac tcc tca agt cca gaa aat aaa agt tta gaa gtt agt gat aca 538

Pro Asp Ser Ser Ser Pro Glu Asn Lys Ser Leu Glu Val Ser Asp Thr

150

155

160

cgt ttt cac agt ttt tca ttt tat gaa ttg aag aat gtc aca aat aac 586

Arg Phe His Ser Phe Ser Phe Tyr Glu Leu Lys Asn Val Thr Asn Asn

165

170

175

ttt Phe 180	gat Asp	gaa Glu	cga Arg	ccc Pro	att Ile 185	tct Ser	gtt Val	ggt Gly	ggt Gly	aat Asn 190	aaa Lys	atg Met	gga Gly	gag Glu	gga Gly 195	634
gga Gly	ttt Phe	gga Gly	gtt Val	gta Val 200	tat Tyr	aaa Lys	ggc Gly	tac Tyr	gta Val 205	aat Asn	aac Asn	aca Thr	act Thr	gtg Val 210	gca Ala	682
gtg Val	aag Lys	aag Lys	ctt Leu 215	gca Ala	gca Ala	atg Met	gtt Val	gac Asp 220	att Ile	act Thr	act Thr	gaa Glu 225	gaa Glu	ctg Leu	aaa Lys	730
cag Gln	cag Gln	ttt Phe 230	gat Asp	caa Gln	gaa Glu	ata Ile	aaa Lys 235	gta Val	atg Met	gca Ala	aag Lys	tgt Cys 240	caa Gln	cat His	gaa Glu	778
aac Asn 245	tta Leu	gta Val	gaa Glu	cta Leu	ctt Leu	ggt Gly 250	ttc Phe	tca Ser	agt Ser	gat Asp	gga Gly 255	gat Asp	gac Asp	ctc Leu	tgc Cys	826
tta Leu 260	gta Val	tat Tyr	gtt Val	tac Tyr	atg Met 265	cct Pro	aat Asn	ggt Gly	tca Ser	ttg Leu 270	cta Leu	gac Asp	aga Arg	ctc Leu	tct Ser 275	874
tgc Cys	ttg Leu	gat Asp	ggt Gly 280	act Thr	cca Pro	cca Pro	ctt Leu	tct Ser	tgg Trp 285	cac His	atg Met	aga Arg	tgc Cys 290	aag Lys	att Ile	922
gct Ala 295	cag Gln	ggt Gly	gca Ala	gct Ala	aat Asn	ggc Gly	atc Ile	aat Asn 300	ttt Phe	cta Leu	cat His	gaa Glu 305	aat Asn	cat His	cat His	970
att Ile	cat His 310	aga Arg	gat Asp	att Ile	aaa Lys	agt Ser	gca Ala 315	aat Asn	atc Ile	tta Leu	ctg Leu 320	gat Asp	gaa Glu	gct Ala	ttt Phe	1018
act Thr 325	gct Ala	aaa Lys	ata Ile	tct Ser	gac Asp	ttt Phe 330	ggc Gly	ctt Leu	gca Ala	cgg Arg 335	gct Ala 335	tct Ser	gag Glu	aag Lys	ttt Phe	1066
gcc Ala 340	cag Gln	aca Thr	gtc Val	atg Met	act Thr 345	agc Ser	aga Arg	att Ile	gtg Val 350	gga Gly 350	aca Thr	aca Thr	gct Ala	tat Tyr	atg Met 355	1114
gca Ala	cca Pro	gaa Glu	gct Ala	ttg Leu 360	cgt Arg	gga Gly	gaa Glu	ata Ile	aca Thr 365	ccc Pro	aaa Lys	tct Ser	gat Asp	att Ile 370	tac Tyr	1162
agc Ser	ttt Phe	ggt Gly	gtg Val 375	gtt Val	tta Leu	cta Leu	gaa Glu	ata Ile 380	ata Ile	act Thr	gga Gly	ctt Leu	cca Pro 385	gct Ala	gtg Val	1210
gat Asp	gaa Glu	cac His 390	cgt Arg	gaa Glu	cct Pro	cag Gln	tta Leu 395	ttg Leu	cta Leu	gat Asp	att Ile 400	aaa Lys	gaa Glu	gaa Glu	att Ile	1258

gaa gat gaa gaa aag aca att gaa gat tat att gat aaa aag atg aat 1306
 Glu Asp Glu Glu Lys Thr Ile Glu Asp Tyr Ile Asp Lys Lys Met Asn
 405 410 415

gat gct gat tcc act tca gtt gaa gct atg tac tct ggt gct agc caa 1354
 Asp Ala Asp Ser Thr Ser Val Glu Ala Met Tyr Ser Gly Ala Ser Gln
 420 425 430 435

tgt cgg cat gaa aag aaa aat aag agc cca gac att aag aag gtt cac 1402
 Cys Arg His Glu Lys Lys Asn Lys Ser Pro Asp Ile Lys Lys Val His
 440 445 450

cag ctg ctg caa gag atg aca gct tct taaaacttta ttgaaaaaga 1449
 Gln Leu Leu Gln Glu Met Thr Ala Ser
 455 460

ctcttgactt tttatataca cctatctcaa ccattttttt aactgatttt tttcctaaat 1509
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 gttgaacttc caaaatataa aaatagagcc accatatcaa cacttagccc taccattag 1629
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<210> 28
 <211> 460
 <212> PRT
 <213> Homo sapien

<400> 28
 Met Asn Lys Pro Ile Thr Pro Ser Thr Tyr Val Arg Cys Leu Asn Val
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 Gly Leu Ile Arg Lys Leu Ser Asp Phe Ile Asp Pro Gln Glu Gly Trp
 20 25 30
 Lys Lys Leu Ala Val Ala Ile Lys Pro Ser Gly Asp Asp Arg Tyr
 35 40 45
 Asn Gln Phe His Ile Arg Arg Phe Glu Ala Leu Leu Gln Thr Gly Lys
 50 55 60

Ser	Pro	Thr	Ser	Glu	Leu	Leu	Phe	Asp	Trp	Gly	Thr	Thr	Asn	Cys	Thr
65				70						75					80
Val	Gly	Asp	Leu	Val	Asp	Leu	Leu	Ile	Gln	Asn	Glu	Phe	Phe	Ala	Pro
			85						90					95	
Ala	Ser	Leu	Leu	Leu	Pro	Asp	Ala	Val	Pro	Lys	Thr	Ala	Asn	Thr	Leu
			100					105					110		
Pro	Ser	Lys	Glu	Ala	Ile	Thr	Val	Gln	Gln	Lys	Gln	Met	Pro	Phe	Cys
		115					120					125			
Asp	Lys	Asp	Arg	Thr	Leu	Met	Thr	Pro	Val	Gln	Asn	Leu	Glu	Gln	Ser
	130					135					140				
Tyr	Met	Pro	Pro	Asp	Ser	Ser	Ser	Pro	Glu	Asn	Lys	Ser	Leu	Glu	Val
145					150					155					160
Ser	Asp	Thr	Arg	Phe	His	Ser	Phe	Ser	Phe	Tyr	Glu	Leu	Lys	Asn	Val
				165					170					175	
Thr	Asn	Asn	Phe	Asp	Glu	Arg	Pro	Ile	Ser	Val	Gly	Gly	Asn	Lys	Met
			180					185					190		
Gly	Glu	Gly	Gly	Phe	Gly	Val	Val	Tyr	Lys	Gly	Tyr	Val	Asn	Asn	Thr
		195					200					205			
Thr	Val	Ala	Val	Lys	Lys	Leu	Ala	Ala	Met	Val	Asp	Ile	Thr	Thr	Glu
	210					215					220				
Glu	Leu	Lys	Gln	Gln	Phe	Asp	Gln	Glu	Ile	Lys	Val	Met	Ala	Lys	Cys
225					230					235					240
Gln	His	Glu	Asn	Leu	Val	Glu	Leu	Leu	Gly	Phe	Ser	Ser	Asp	Gly	Asp
				245					250					255	
Asp	Leu	Cys	Leu	Val	Tyr	Val	Tyr	Met	Pro	Asn	Gly	Ser	Leu	Leu	Asp
			260					265					270		
Arg	Leu	Ser	Cys	Leu	Asp	Gly	Thr	Pro	Pro	Leu	Ser	Trp	His	Met	Arg
		275					280					285			
Cys	Lys	Ile	Ala	Gln	Gly	Ala	Ala	Asn	Gly	Ile	Asn	Phe	Leu	His	Glu
	290					295					300				
Asn	His	His	Ile	His	Arg	Asp	Ile	Lys	Ser	Ala	Asn	Ile	Leu	Leu	Asp
305					310					315					320
Glu	Ala	Phe	Thr	Ala	Lys	Ile	Ser	Asp	Phe	Gly	Leu	Ala	Arg	Ala	Ser
				325					330					335	
Glu	Lys	Phe	Ala	Gln	Thr	Val	Met	Thr	Ser	Arg	Ile	Val	Gly	Thr	Thr
			340					345					350		
Ala	Tyr	Met	Ala	Pro	Glu	Ala	Leu	Arg	Gly	Glu	Ile	Thr	Pro	Lys	Ser
		355					360					365			
Asp	Ile	Tyr	Ser	Phe	Gly	Val	Leu	Leu	Glu	Ile	Ile	Thr	Gly	Leu	
	370					375					380				
Pro	Ala	Val	Asp	Glu	His	Arg	Glu	Pro	Gln	Leu	Leu	Asp	Ile	Lys	
385					390					395					400
Glu	Glu	Ile	Glu	Asp	Glu	Glu	Lys	Thr	Ile	Glu	Asp	Tyr	Ile	Asp	Lys
				405					410					415	
Lys	Met	Asn	Asp	Ala	Asp	Ser	Thr	Ser	Val	Glu	Ala	Met	Tyr	Ser	Gly
			420					425					430		
Ala	Ser	Gln	Cys	Arg	His	Glu	Lys	Lys	Asn	Lys	Ser	Pro	Asp	Ile	Lys
		435					440					445			
Lys	Val	His	Gln	Leu	Leu	Gln	Glu	Met	Thr	Ala	Ser				
	450					455					460				

<210> 29
 <211> 142
 <212> PRT

<213> Homo sapien

<400> 29

Lys	Leu	Lys	Gly	Glu	Pro	Gly	Trp	Val	Thr	Ile	His	Gly	Met	Ala	Gly	
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Cys	Gly	Lys	Ser	Val	Leu	Ala	Ala	Glu	Ala	Val	Arg	Asp	His	Ser	Leu	
		20						25					30			
Leu	Glu	Gly	Cys	Phe	Pro	Gly	Gly	Val	His	Trp	Val	Ser	Val	Gly	Lys	
		35					40						45			
Gln	Asp	Lys	Ser	Gly	Leu	Leu	Met	Lys	Leu	Gln	Asn	Leu	Cys	Thr	Arg	
	50					55					60					
Leu	Asp	Gln	Asp	Glu	Ser	Phe	Ser	Gln	Arg	Leu	Pro	Leu	Asn	Ile	Glu	
65					70					75					80	
Glu	Ala	Lys	Asp	Arg	Leu	Arg	Ile	Leu	Met	Leu	Arg	Lys	His	Pro	Arg	
			85						90					95		
Ser	Leu	Leu	Ile	Leu	Asp	Asp	Val	Trp	Asp	Ser	Trp	Val	Leu	Lys	Ala	
			100					105					110			
Phe	Asp	Ser	Gln	Cys	Gln	Ile	Leu	Leu	Thr	Thr	Arg	Asp	Lys	Ser	Val	
		115					120					125				
Thr	Asp	Ser	Val	Met	Gly	Pro	Lys	Tyr	Val	Val	Pro	Val	Glu			
	130					135						140				

<210> 30

<211> 145

<212> PRT

<213> C. elegans

<400> 30

Glu	Met	Cys	Asp	Leu	Asp	Ser	Phe	Phe	Leu	Phe	Leu	His	Gly	Arg	Ala	
1				5					10					15		
Gly	Ser	Gly	Lys	Ser	Val	Ile	Ala	Ser	Gln	Ala	Leu	Ser	Lys	Ser	Asp	
			20					25					30			
Gln	Leu	Ile	Gly	Ile	Asn	Tyr	Asp	Ser	Ile	Val	Trp	Leu	Lys	Asp	Ser	
		35					40						45			
Gly	Thr	Ala	Pro	Lys	Ser	Thr	Phe	Asp	Leu	Phe	Thr	Asp	Ile	Leu	Leu	
	50					55					60					
Met	Leu	Lys	Ser	Glu	Asp	Asp	Leu	Leu	Asn	Phe	Pro	Ser	Val	Glu	His	
65					70					75					80	
Val	Thr	Ser	Val	Val	Leu	Lys	Arg	Met	Ile	Cys	Asn	Ala	Leu	Ile	Asp	
				85					90					95		
Arg	Pro	Asn	Thr	Leu	Phe	Val	Phe	Asp	Asp	Val	Val	Gln	Glu	Glu	Thr	
			100					105					110			
Ile	Arg	Trp	Ala	Gln	Glu	Leu	Arg	Leu	Arg	Cys	Leu	Val	Thr	Thr	Arg	
		115					120					125				
Asp	Val	Glu	Ile	Ser	Asn	Ala	Ala	Ser	Gln	Thr	Cys	Glu	Phe	Ile	Glu	
	130					135						140				
Val																
145																

<210> 31

<211> 75

<212> PRT

<213> Homo sapien

<400> 31

Met Asp Phe Ser Arg Asn Leu Tyr Asp Ile Gly Glu Gln Leu Asp Ser
1 5 10 15
Glu Asp Leu Ala Ser Leu Lys Phe Leu Ser Leu Asp Tyr Ile Pro Gln
20 25 30
Arg Lys Gln Glu Pro Ile Lys Asp Ala Leu Met Leu Phe Gln Arg Leu
35 40 45
Gln Glu Lys Arg Met Leu Glu Glu Ser Asn Leu Ser Phe Leu Lys Glu
50 55 60
Leu Leu Phe Arg Ile Asn Arg Leu Asp Leu Leu
65 70 75

<210> 32

<211> 76

<212> PRT

<213> Homo sapien

<400> 32

His Leu Leu Ile Arg Val Met Leu Tyr Gln Ile Ser Glu Glu Val Ser
1 5 10 15
Arg Ser Glu Leu Arg Ser Phe Lys Phe Leu Leu Gln Glu Glu Ile Ser
20 25 30
Lys Cys Lys Leu Asp Asp Asp Met Asn Leu Leu Asp Ile Phe Ile Glu
35 40 45
Met Glu Lys Arg Val Ile Leu Gly Glu Gly Lys Leu Asp Ile Leu Lys
50 55 60
Arg Val Cys Ala Gln Ile Asn Lys Ser Leu Leu Lys
65 70 75

<210> 33

<211> 77

<212> PRT

<213> Homo sapien

<400> 33

Lys Val Ser Phe Arg Glu Lys Leu Leu Ile Ile Asp Ser Asn Leu Gly
1 5 10 15
Val Gln Asp Val Glu Asn Leu Lys Phe Leu Cys Ile Gly Leu Val Pro
20 25 30
Asn Lys Lys Leu Glu Lys Ser Ser Ala Ser Asp Val Phe Glu His
35 40 45
Leu Leu Ala Glu Asp Leu Leu Ser Glu Glu Asp Pro Phe Phe Leu Ala
50 55 60
Glu Leu Leu Tyr Ile Ile Arg Gln Lys Lys Leu Leu Gln
65 70 75

<210> 34

<211> 72

<212> PRT

<213> Homo sapien

<400> 34

Val Ser Leu Phe Arg Asn Leu Leu Tyr Glu Leu Ser Glu Gly Ile Asp
1 5 10 15
Ser Glu Asn Leu Lys Asp Met Ile Phe Leu Leu Lys Asp Ser Leu Pro
20 25 30
Lys Thr Glu Met Thr Ser Leu Ser Phe Leu Ala Phe Leu Glu Lys Gln
35 40 45
Gly Lys Ile Asp Glu Asp Asn Leu Thr Cys Leu Glu Asp Leu Cys Lys
50 55 60
Thr Val Val Pro Lys Leu Leu Arg
65 70

<210> 35

<211> 77

<212> PRT

<213> Homo sapien

<400> 35

Met Asp Pro Phe Leu Val Leu Leu His Ser Val Ser Ser Ser Leu Ser
1 5 10 15
Ser Ser Glu Leu Thr Glu Leu Lys Phe Leu Cys Leu Gly Arg Val Gly
20 25 30
Lys Arg Lys Leu Glu Arg Val Gln Ser Gly Leu Asp Leu Phe Ser Met
35 40 45
Leu Leu Glu Gln Asn Asp Leu Glu Pro Gly His Thr Glu Leu Leu Arg
50 55 60
Glu Leu Leu Ala Ser Leu Arg Arg His Asp Leu Leu Arg
65 70 75

<210> 36

<211> 99

<212> PRT

<213> Homo sapien

<400> 36

Trp Pro Glu Glu His Gly Glu Gln Glu His Gly Leu Tyr Ser Leu His
1 5 10 15
Arg Met Phe Asp Ile Val Gly Thr His Leu Thr His Arg Asp Val Arg
20 25 30
Val Leu Ser Phe Leu Phe Val Asp Val Ile Asp His Glu Arg Gly Leu
35 40 45
Ile Arg Asn Gly Arg Asp Phe Leu Leu Ala Leu Glu Arg Gln Gly Arg
50 55 60
Cys Asp Glu Ser Asn Phe Arg Gln Val Leu Gln Leu Leu Arg Ile Ile
65 70 75 80
Thr Arg His Asp Leu Leu Pro Tyr Val Thr Leu Lys Arg Arg Arg Ala
85 90 95
Val Cys Pro

<210> 37

<211> 99

<212> PRT
 <213> Mus musculus

<400> 37
 Trp Pro Glu Glu Arg Gly Glu Gln Glu His Gly Leu Tyr Ser Leu His
 1 5 10 15
 Arg Met Phe Asp Ile Val Gly Thr His Leu Thr His Arg Asp Val Arg
 20 25 30
 Val Leu Ser Phe Leu Phe Val Asp Val Ile Asp His Glu Arg Gly Leu
 35 40 45
 Ile Arg Asn Gly Arg Asp Phe Leu Leu Ala Leu Glu Arg Gln Gly Arg
 50 55 60
 Cys Asp Glu Ser Asn Phe Arg Gln Val Leu Gln Leu Leu Arg Ile Ile
 65 70 75 80
 Thr Arg His Asp Leu Leu Pro Tyr Val Thr Leu Lys Lys Arg Arg Ala
 85 90 95
 Val Cys Pro

<210> 38
 <211> 146
 <212> PRT
 <213> Danio rerio

<400> 38
 Trp Glu Glu Thr Glu Cys Leu Ser Tyr Tyr Glu Thr Leu Ser Leu His
 1 5 10 15
 Glu Ile Phe Glu Ile Val Gly Ser Gln Leu Thr Glu Thr Cys Gly Gly
 20 25 30
 Glu Val Ala Phe Leu Leu Asp Glu Thr Tyr Pro Gly Lys His Pro Leu
 35 40 45
 Asp Pro Glu Gly Trp Thr Glu Asp Leu Pro Pro Gly Pro Asp Gly Ser
 50 55 60
 Pro Gln Ala Asn Thr Pro Cys Pro Arg Leu Leu Lys Ser Trp Gln Arg
 65 70 75 80
 Met Gln Pro Gln Lys Glu Gly Cys Ser Ile Ala Ser Arg His Arg Pro
 85 90 95
 Lys Ser Gly Val Glu Leu Leu Leu Glu Glu Arg Arg Gly Tyr Leu
 100 105 110
 Ser Asp Ala Asn Leu Arg Pro Leu Leu Gln Leu Leu Arg Ile Leu Thr
 115 120 125
 Arg His Asp Val Leu Pro Phe Val Ser Gln Lys Lys Arg Arg Thr Val
 130 135 140
 Ser Pro
 145

<210> 39
 <211> 82
 <212> PRT
 <213> Homo sapien

<400> 39
 Met Asp Pro Phe Leu Val Leu Leu His Ser Val Ser Ser Ser Leu Ser

1	5	10	15
Ser Ser Glu Leu Thr Glu Leu Lys Tyr Leu Cys Leu Gly Arg Lys Arg			
20	25	30	
Lys Leu Glu Arg Val Gln Ser Gly Leu Asp Leu Phe Ser Met Leu Leu			
35	40	45	
Glu Gln Asn Asp Leu Glu Pro Gly His Thr Glu Leu Leu Arg Glu Leu			
50	55	60	
Leu Ala Ser Leu Arg Arg His Asp Leu Leu Arg Arg Val Asp Asp Phe			
65	70	75	80
Glu Leu			

<210> 40
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> oligonucleotide

<400> 40
 atgatgctga aaggaata 18

<210> 41
 <211> 40
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> oligonucleotide

<400> 41
 agtcctcgac tcacgtgcaa ggatgatgct gaaaggaata 40

<210> 42
 <211> 35
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic primer

<400> 42
 gcgaattcat gaacaaaccc ataacaccat caaca 35

<210> 43
 <211> 35
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic primer

<400> 43

gcctcgagtt aagaagctgt catctcttgc agcag

35

<210> 44

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic primer

<400> 44

atgatggagg tgtttatg

18

<210> 45

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic primer

<400> 45

ataagattga tgacaactac

20

<210> 46

<211> 16

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic primer

<400> 46

ctccgccgcc gtctgg

16

<210> 47

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic primer

<400> 47

cgcccaggag tcatcggacg c

21

<210> 48

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic primer

<400> 48

23

<211> 28

<213> Art:

<213> Artificial Sequence

<223> synthetic primer

acacccggac cttgcctgcc agctttac

28

<211> 18

<212> DNA

<213> Artificial Sequence

<223> synthetic primer

atgctttata acgtcagc

18

<211> 21

<212> DNA

<213> Artificial Sequence

<223> synthetic primer

tcacaccacc gaggagctct c

21

<211> 195

<212> DNA

<213> C. muridarum

<221> CDS

<222> (1) ... (195)

gat tta tgg aaa caa ttt gtg ttt gct ctt gga gtg tct tca gaa gag 48

Asp Leu Trp Lys Gln Phe Val Phe Ala Leu Gly Val Ser Ser Glu Glu
1 5 10 15

cta gaa qct cat gaa ccc agt gaa qca qct aaa qct aaq gtt gcg aca 96

Leu Glu Ala His Glu Pro Ser Glu Ala Lys Ala Lys Val Ala Thr

ttt atg cgg tgg tgc aca ggg gat tct tta gca gca gga gta gcg gct 144

Phe Met Arg Trp Cys Thr Gly Asp Ser Leu Ala Ala Gly Val Ala Ala

35

40

45

ttg tat tct tat gaa agt caa att cct tgc gta gct aaa gaa aaa att 192
 Leu Tyr Ser Tyr Glu Ser Gln Ile Pro Cys Val Ala Lys Glu Lys Ile
 50 55 60

cgt 195
 Arg
 65

<210> 53
 <211> 65
 <212> PRT
 <213> C. muridarum

<400> 53
 Asp Leu Trp Lys Gln Phe Val Phe Ala Leu Gly Val Ser Ser Glu Glu
 1 5 10 15
 Leu Glu Ala His Glu Pro Ser Glu Ala Ala Lys Ala Lys Val Ala Thr
 20 25 30
 Phe Met Arg Trp Cys Thr Gly Asp Ser Leu Ala Ala Gly Val Ala Ala
 35 40 45
 Leu Tyr Ser Tyr Glu Ser Gln Ile Pro Cys Val Ala Lys Glu Lys Ile
 50 55 60
 Arg
 65

<210> 54
 <211> 711
 <212> DNA
 <213> C. muridarum

<220>
 <221> CDS
 <222> (1)...(708)

<400> 54
 atg gaa tca aga aaa gga ata aaa gag gtg agc atg aat ttt tta gat 48
 Met Glu Ser Arg Lys Gly Ile Lys Glu Val Ser Met Asn Phe Leu Asp
 1 5 10 15
 cag cta gat gca att att caa aac aaa cat atg tta gaa cac cct ttt 96
 Gln Leu Asp Ala Ile Ile Gln Asn Lys His Met Leu Glu His Pro Phe
 20 25 30
 tac atg aag tgg tca aaa gga gag ctg aca aaa gaa caa tta cag gca 144
 Tyr Met Lys Trp Ser Lys Gly Glu Leu Thr Lys Glu Gln Leu Gln Ala
 35 40 45
 tac gca aaa gat tac tat ttg cat atc aaa gct ttt cca aaa tat tta 192
 Tyr Ala Lys Asp Tyr Tyr Leu His Ile Lys Ala Phe Pro Lys Tyr Leu
 50 55 60

tct gct att cat agc cgt tgt gat gat tta gaa gcc cgc aag tta tta	240
Ser Ala Ile His Ser Arg Cys Asp Asp Leu Glu Ala Arg Lys Leu Leu	
65 70 75 80	
tta gat aac tta atg gat gaa gag aat ggt tat cct aat cat att gat	288
Leu Asp Asn Leu Met Asp Glu Glu Asn Gly Tyr Pro Asn His Ile Asp	
85 90 95	
tta tgg aaa caa ttt gtg ttt gct ctt gga gtg tct tca gaa gag cta	336
Leu Trp Lys Gln Phe Val Phe Ala Leu Gly Val Ser Ser Glu Glu Leu	
100 105 110	
gaa gct cat gaa ccc agt gaa gca gct aaa gct aag gtt gcg aca ttt	384
Glu Ala His Glu Pro Ser Glu Ala Ala Lys Ala Lys Val Ala Thr Phe	
115 120 125	
atg cgg tgg tgc aca ggg gat tct tta gca gca gga gta gcg gct ttg	432
Met Arg Trp Cys Thr Gly Asp Ser Leu Ala Ala Gly Val Ala Ala Leu	
130 135 140	
tat tct tat gaa agt caa att cct tgc gta gct aaa gaa aaa att cgt	480
Tyr Ser Tyr Glu Ser Gln Ile Pro Cys Val Ala Lys Glu Lys Ile Arg	
145 150 155 160	
gga ttg att gag tac ttt ggc ttt tct aat cct gaa gat tat gct tat	528
Gly Leu Ile Glu Tyr Phe Gly Phe Ser Asn Pro Glu Asp Tyr Ala Tyr	
165 170 175	
ttc acg gag cat gaa gaa gct gat gtg cgt cat gct agg gaa gaa aag	576
Phe Thr Glu His Glu Glu Ala Asp Val Arg His Ala Arg Glu Glu Lys	
180 185 190	
gcc tta att gag atg ttg tct aga gat gat agc gac aaa gtt tta gaa	624
Ala Leu Ile Glu Met Leu Ser Arg Asp Asp Ser Asp Lys Val Leu Glu	
195 200 205	
gct tcg cga gaa gtt aca caa tct tta tac ggc ttt ttg gat tca ttt	672
Ala Ser Arg Glu Val Thr Gln Ser Leu Tyr Gly Phe Leu Asp Ser Phe	
210 215 220	
tta gag cct gca aca tgt tgt cat tgt cac aaa gct taa	711
Leu Glu Pro Ala Thr Cys Cys His Cys His Lys Ala	
225 230 235	

<210> 55
 <211> 236
 <212> PRT
 <213> C. muridarum

<400> 55
 Met Glu Ser Arg Lys Gly Ile Lys Glu Val Ser Met Asn Phe Leu Asp
 1 5 10 15
 Gln Leu Asp Ala Ile Ile Gln Asn Lys His Met Leu Glu His Pro Phe
 20 25 30

Tyr Met Lys Trp Ser Lys Gly Glu Leu Thr Lys Glu Gln Leu Gln Ala
 35 40 45
 Tyr Ala Lys Asp Tyr Tyr Leu His Ile Lys Ala Phe Pro Lys Tyr Leu
 50 55 60
 Ser Ala Ile His Ser Arg Cys Asp Asp Leu Glu Ala Arg Lys Leu Leu
 65 70 75 80
 Leu Asp Asn Leu Met Asp Glu Glu Asn Gly Tyr Pro Asn His Ile Asp
 85 90 95
 Leu Trp Lys Gln Phe Val Phe Ala Leu Gly Val Ser Ser Glu Glu Leu
 100 105 110
 Glu Ala His Glu Pro Ser Glu Ala Ala Lys Ala Lys Val Ala Thr Phe
 115 120 125
 Met Arg Trp Cys Thr Gly Asp Ser Leu Ala Ala Gly Val Ala Ala Leu
 130 135 140
 Tyr Ser Tyr Glu Ser Gln Ile Pro Cys Val Ala Lys Glu Lys Ile Arg
 145 150 155 160
 Gly Leu Ile Glu Tyr Phe Gly Phe Ser Asn Pro Glu Asp Tyr Ala Tyr
 165 170 175
 Phe Thr Glu His Glu Glu Ala Asp Val Arg His Ala Arg Glu Glu Lys
 180 185 190
 Ala Leu Ile Glu Met Leu Ser Arg Asp Asp Ser Asp Lys Val Leu Glu
 195 200 205
 Ala Ser Arg Glu Val Thr Gln Ser Leu Tyr Gly Phe Leu Asp Ser Phe
 210 215 220
 Leu Glu Pro Ala Thr Cys Cys His Cys His Lys Ala
 225 230 235

<210> 56
 <211> 65
 <212> PRT
 <213> C. pneumoniae

<400> 56
 Asp Leu Trp Arg Gln Phe Ala Leu Ser Leu Gly Val Ser Glu Glu Glu
 1 5 10 15
 Leu Ala Asn His Glu Phe Ser Gln Ala Gln Asp Met Val Ala Thr
 20 25 30
 Phe Arg Arg Leu Cys Asp Met Pro Gln Leu Ala Val Gly Leu Gly Ala
 35 40 45
 Leu Tyr Thr Tyr Glu Ile Gln Ile Pro Gln Val Cys Val Glu Lys Ile
 50 55 60
 Arg
 65

<210> 57
 <211> 224
 <212> PRT
 <213> C. pneumoniae

<400> 57
 Met Thr Ser Trp Ile Glu Leu Leu Asp Lys Gln Ile Glu Asp Gln His
 1 5 10 15
 Met Leu Lys His Glu Phe Tyr Gln Arg Trp Ser Glu Gly Lys Leu Glu

